CLAIMS

1. An enzyme comprising cellulolytic activity comprising an amino acid sequence comprising an amino acid string selected from the group consisting of one or more of the following:

(a) Asn-Asn-(Leu/Phe/Lys/Ile)-Trp-Gly

(b) Glu-(Leu/Phe/Ile)-Met-Ile-Trp

(c) Gly-Thr-Glu-Pro-Phe-Thr;

(d) (Ser/Tyr/Cys/Trp/Thr/Asn/Lys/Arg)-(Val/Pro)-(Lys/Ala)-(Ser/Ala)-(Tyr/Phe); and

(e) Lys-Asn-Phe-Phe-Asn-Tyr

or a derivative of said enzyme.

2. The enzyme according to claim 1, said cellulase being derived from a fungus, bacteria or Actinomycete.

3. The enzyme according to claim 1, wherein said enzyme is an endoglucanase.

4. The enzyme according to claim 2, wherein said fungus is a filamentous fungus.

5. The enzyme according to claim 4, wherein said filamentous fungus belongs to Euascomycete.

6. The enzyme according to claim 5, wherein said Euascomycete belongs to Plectomycete.

7. The enzyme according to claim 5, wherein said Euascomycete belongs to Diaporthales, Halosphaeriales, Microascales, Ophiostomatales, Phyllachorales, Sordariales or Xylariales.

8. The enzyme according to claim 5, wherein said Eusacomycete belongs to Hypocreales comprising Clavicipitaceae, Melanosporaceae, Nectriaceae, Niessliaceae or Mitosporic Hypocreales.

9. The enzyme according to claim 5, wherein said Euascomycete belongs to Hypocreaceae, wherein said Hypocreaceae does not comprise Trichoderma.

10. The enzyme according to claim 5, wherein said Euascomycete is *Gliocladium spp., Fusarium spp., Acremonium spp., Myceliophtora spp., Verticillium spp., Myrothecium spp.,* or *Penicillium spp.*

11. The enzyme according to claim 5, wherein said Euascomycete is an *Aspergillus* comprising *A. aeneus, A. anthodesmis, A. aureofulgens, A. aureolatus, A. avenaceus, A. awamorii, A. bisporus, A. brunneouniseriatus, A. campestris, A. caesiellus, A. candidus, A. carbonarius, A. carneus, A. cervinus, A. clavatoflavus, A. clavatoanicus, A. clavatus, A. conicus, A. conjunctus, A. crustosus, A. deflectus, A. dimorphicus, A. eburneocremeus, A. egyptiacus, A. ellipticus, A. elongatus, A. ficuum, A. flaschentraegeri, A. flavus, a. fumigatus, A. giganteus, A. glaucus, A. gorakhpurensis, A. gracilis, A. iizuke, A. itaconicus, A. japonicus, A. kambarensis, A. kanagawaensis, A. lanosus, A. leporis, A. longivesica, A. mellinus, A. multicolor, A. niger, A. nomius, A. nutans, A. ochraceus, A. oryzae, A. pallidus, A. panamensis, A. parasiticus, A. parvulus, A. penicillioides, A. phialisepticus, A. phoenicis, A. proliferans, A.pulvinus, A.puniceus, A.raperi, A.recurvatus, A.restrictus, A.shirousami, A.sojae, A.sparsus, A. subolivaceus, A.subsessilis, A.tamarii, A.terreus, A.terricola, A. thomii, A.tubingensis, A. unguis, A.unilateralis, A.ustus, A.versicolor, A.wentii, A.xerophilus, A.zonatus, A.sp.*

12. The enzyme according to claim 1, wherein said enzyme has an amino acid sequence identity with that of EGIII of greater than 30%.

13. The enzyme according to claim 12, wherein said enzyme has an amino acid sequence identity with that of EGIII of greater than 60%.

14. A DNA encoding the enzyme according to claim 1.

15. A vector comprising the DNA of claim 14.

16. A host cell transformed with the vector of claim 15.

17. A method of producing a cellulase comprising the steps of:

(a) culturing the host cell according to claim 16 in a suitable culture medium under suitable conditions to produce cellulase;

(b) obtaining said produced cellulase; and optionally

(c) purifying said cellulase to provide a purified cellulase product.

18. A method for obtaining a gene encoding an EGIII like cellulase comprising the steps of

(a) preparing genomic DNA from an organism of interest;

(b) preparing a DNA primer encoding an amino acid string selected from the group consisting of one or more of the following:

(a) Asn-Asn-(Leu/Phe/Lys/Ile)-Trp-Gly

(b) Glu-(Leu/Phe/Ile)-Met-Ile-Trp

(c) Gly-Thr-Glu-Pro-Phe-Thr;

(d) (Ser/Tyr/Cys/Trp/Thr/Asn/Lys/Arg)-(Val/Pro)-(Lys/Ala)-(Ser/Ala)-(Tyr/Phe); and

(e) Lys-Asn-Phe-Phe-Asn-Tyr.

(c) mixing said genomic DNA from step (a) and said DNA primer from step (b) under conditions suitable for the identification of all or part of a gene fragment in said genomic DNA corresponding to said DNA primer; and

(d) isolating said all or part of said gene corresponding to said fragment from said genomic DNA.

19. The method according to claim 18, wherein said step (c) further comprises labeling said DNA primer and performing hybridization between said labeled DNA primer and said genomic DNA and detecting said hybridized genomic DNA which encodes all or part of an EGIII like cellulase.

20. The method according to claim 18, wherein, said step (c) further comprises initiating a PCR reaction between said DNA primer and said genomic DNA and identifying a resulting amplified DNA fragment which comprises all or part of a gene encoding an EGIII like cellulase.

21. The method according to claim 18, wherein said genomic DNA is obtained from a bacteria, fungus or Actinomycete.

22. A vector comprising the gene isolated according to claim 18.

23. A host cell transformed with the vector of claim 22.

24. An EGIII like cellulase encoded by the gene obtained according to claim 18.

25. The use of the EGIII like cellulase according to claim 24 in the treatment of a cellulose containing textile.

26. The use of the EGIII like cellulase according to claim 24 as a feed additive.

27. The use of the EGIII like cellulase according to claim 24 in the treatment of wood pulp.

28. The use of the EGIII like cellulase according to claim 24 in the reduction of biomass to glucose. The use of the EGIII like cellulase according to claim 24 in the stonewashing or indigo dyed denim.

29. A laundry detergent comprising the EGIII like cellulase according to claim 24.

Add a17